

P4/10

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/509,422

CRF Edit Date: 10/6/04  
Edited by: Ma

Realigned nucleic acid/ amino acid numbers text in cases where the sequence text "wrapped" to the next line

**ENTERED**

Corrected the SEQ ID NO. Sequence numbers edited were:

3,4

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

Deleted: \_\_\_\_\_ invalid beginning/end-of-file text ; \_\_\_\_\_ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

Other:

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,422

DATE: 10/06/2004

TIME: 16:26:11

Input Set : A:\pto.amc.TXT

Output Set: N:\CRF4\10062004\J509422.raw

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6 <110> APPLICANT: Liou, Simon
8 <120> TITLE OF INVENTION: Human BMP2 Inducible Kinases
10 <130> FILE REFERENCE: 004974.01015
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/509,422
C--> 12 <141> CURRENT FILING DATE: 2004-09-24
12 <150> PRIOR APPLICATION NUMBER: PCT/EP03/080825
13 <151> PRIOR FILING DATE: 2003-03-20
15 <150> PRIOR APPLICATION NUMBER: US 60/367,512
16 <151> PRIOR FILING DATE: 2002-03-27
18 <150> PRIOR APPLICATION NUMBER: US 60/406,936
19 <151> PRIOR FILING DATE: 2002-08-30
21 <160> NUMBER OF SEQ ID NOS: 9
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3507
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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32 ggcggggctg ggcggggccg ggccggggcc ggctgcggct ccggcgccgc gtccgtgggg      120
33 gtccgggtgt tcgcggtcgg ccgccaccag gtcaccctgg aagagtcgct ggccgaaggt      180
34 ggattctcca cagttttcct cgtgcgtact cacgggtgaa tccgatgtgc attgaagcga      240
35 atgtatgtca ataacatgcc agacctcaat gtttgtaaaa gggaaattac aattatgaaa      300
36 gagctatctg gtcacaaaaa tattgtgggc tatttggaact gtgctgttaa ttcaattagt      360
37 gataatgtat ggggaagtcct tatcttaatg gaattattgt gagctggaca ggtagtgaat      420
38 caaatgaata agaagctaca gacgggtttt acagaaccag aagtgttaca gatattctgt      480
39 gatacctgtg aagctgttgc aagggttgcag cagtgttaaga ctccaataat tcaccgggat      540
40 ctgaaggtag aaaatatattt gttgaatgat ggtgggaact atgtactttg tgactttggc      600
41 agtgccacta ataaattttct taatcctcaa aaagatggag ttaatgtagt agaagaagaa      660
42 attaaaaagt atacaactct gtcatacaga gccctgaaa tgatcaacct ttatggaggg      720
43 aaacccatca ccaccaaggc tgatatctgg gcactgggat gtctactcta taaactttgt      780
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48 atgactgcta gtgaagcagc tgctaggaaa agccaaataa aagccagaat aacagatacc      1080
49 attggaccaa cagaaacctc aattgcacca agacaaagac caaaggccaa ctctgctact      1140
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51 cctggtgaat tcggttaacca tagacaaaaa ggggcactaa gacctggaaa tggccctgaa      1260
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54 cagcagcagc agcagcagca gcaacagcaa cagcagcagc agcaacagca acagcagcag      1440
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56 atgcagcagt atcaacatgc aacacagcag caacagatgc ttcaacaaca atttttaatg 1560
57 cattcggtat atcaaccaca accttctgca tcacagtatc ctacaatgat gccgcagtat 1620
58 cagcaggctt tctttcaaca gcagatgcta gctcaacatc agccgtctca acaacaggca 1680
59 tcacctgaat atcttacctc cctcaagag ttctcaccag ccttagtttc ctacacttca 1740
60 tcacttccag ctcaggttgg aaccataatg gactctcctt atagtgccaa taggcaagta 1800
61 tttttccagt cagttgctga taaagaggcc attgcaaatt tcacaaatca gaagaacatc 1860
62 agcaatccac ctgatatgtc aggggtggaat ccttttggag aggataattt ctctaagtta 1920
63 acagaagagg aactattgga cagagaattt gaccttctaa gatcaaatag gctcgaggag 1980
64 agagcatcct cagataagaa tgtagactca ctttctgctc cacataacca tcctccagaa 2040
65 gatccttttg gttctgttcc tttcatttct cattcaggca agggttctcc tgaaaagaaa 2100
66 gctgaacatt catctataaa tcaagaaaat ggcactgcaa accctatcaa gaacggtaaa 2160
67 acaagtccag catctaaaga tcagcggact ggaaagaaaa cctcagtaca gggccaagtg 2220
68 caaaagggga atgatgaatc tgaaagtgat tttgaatcag atcccccttc tcctaagagc 2280
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70 gatgatgata ctgaaccaga aaatctgggt cataggcctc tcctcatgga ttctgaagat 2400
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74 gagtttgatg tatttggcgc tgtccccctt tttgcagtgc gtgctcaaca gccccagcaa 2640
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77 gcagtggggc ctgaggcaca tactatcctt ggttatccca aaagtgtaga tgtatttggc 2820
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87 agtgcagatg tattgaaaat ggatgatttt ggtgccgtgc cttttacaga acttgtgggtg 3420
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92 <211> LENGTH: 1168
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 2
97 Met Lys Lys Phe Ser Arg Met Pro Lys Ser Glu Gly Gly Ser Gly Gly
98 1 5 10 15
99 Gly Ala Ala Gly Gly Gly Ala Gly Gly Ala Gly Ala Gly Ala Gly Cys
100 20 25 30
101 Gly Ser Gly Gly Ser Ser Val Gly Val Arg Val Phe Ala Val Gly Arg
102 35 40 45
103 His Gln Val Thr Leu Glu Glu Ser Leu Ala Glu Gly Gly Phe Ser Thr
104 50 55 60
105 Val Phe Leu Val Arg Thr His Gly Gly Ile Arg Cys Ala Leu Lys Arg
106 65 70 75 80

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107 Met Tyr Val Asn Asn Met Pro Asp Leu Asn Val Cys Lys Arg Glu Ile
108      85      90      95
109 Thr Ile Met Lys Glu Leu Ser Gly His Lys Asn Ile Val Gly Tyr Leu
110      100      105      110
111 Asp Cys Ala Val Asn Ser Ile Ser Asp Asn Val Trp Glu Val Leu Ile
112      115      120      125
113 Leu Met Glu Tyr Cys Arg Ala Gly Gln Val Val Asn Gln Met Asn Lys
114      130      135      140
115 Lys Leu Gln Thr Gly Phe Thr Glu Pro Glu Val Leu Gln Ile Phe Cys
116 145      150      155      160
117 Asp Thr Cys Glu Ala Val Ala Arg Leu His Gln Cys Lys Thr Pro Ile
118      165      170      175
119 Ile His Arg Asp Leu Lys Val Glu Asn Ile Leu Leu Asn Asp Gly Gly
120      180      185      190
121 Asn Tyr Val Leu Cys Asp Phe Gly Ser Ala Thr Asn Lys Phe Leu Asn
122      195      200      205
123 Pro Gln Lys Asp Gly Val Asn Val Val Glu Glu Glu Ile Lys Lys Tyr
124      210      215      220
125 Thr Thr Leu Ser Tyr Arg Ala Pro Glu Met Ile Asn Leu Tyr Gly Gly
126 225      230      235      240
127 Lys Pro Ile Thr Thr Lys Ala Asp Ile Trp Ala Leu Gly Cys Leu Leu
128      245      250      255
129 Tyr Lys Leu Cys Phe Phe Thr Leu Pro Phe Gly Glu Ser Gln Val Ala
130      260      265      270
131 Ile Cys Asp Gly Asn Phe Thr Ile Pro Asp Asn Ser Arg Tyr Ser Arg
132      275      280      285
133 Asn Ile His Cys Leu Ile Arg Phe Met Leu Glu Pro Asp Pro Glu His
134      290      295      300
135 Arg Pro Asp Ile Phe Gln Val Ser Tyr Phe Ala Phe Lys Phe Ala Lys
136 305      310      315      320
137 Lys Asp Cys Pro Val Ser Asn Ile Asn Asn Ser Ser Ile Pro Ser Ala
138      325      330      335
139 Leu Pro Glu Pro Met Thr Ala Ser Glu Ala Ala Ala Arg Lys Ser Gln
140      340      345      350
141 Ile Lys Ala Arg Ile Thr Asp Thr Ile Gly Pro Thr Glu Thr Ser Ile
142      355      360      365
143 Ala Pro Arg Gln Arg Pro Lys Ala Asn Ser Ala Thr Thr Ala Thr Pro
144      370      375      380
145 Ser Val Leu Thr Ile Gln Ser Ser Ala Thr Pro Val Lys Val Leu Ala
146 385      390      395      400
147 Pro Gly Glu Phe Gly Asn His Arg Pro Lys Gly Ala Leu Arg Pro Gly
148      405      410      415
149 Asn Gly Pro Glu Ile Leu Leu Gly Gln Gly Pro Pro Gln Gln Pro Pro
150      420      425      430
151 Gln Gln His Arg Val Leu Gln Gln Leu Gln Gln Gly Asp Trp Arg Leu
152      435      440      445
153 Gln Gln Leu His Leu Gln His Arg His Pro His Gln Gln Gln Gln Gln
154      450      455      460
155 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln

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156 465                               470                               475                               480
157 Gln Gln Gln Gln Gln His His His His His His His His Leu Leu
158                               485                               490                               495
159 Gln Asp Ala Tyr Met Gln Gln Tyr Gln His Ala Thr Gln Gln Gln Gln
160                               500                               505                               510
161 Met Leu Gln Gln Gln Phe Leu Met His Ser Val Tyr Gln Pro Gln Pro
162                               515                               520                               525
163 Ser Ala Ser Gln Tyr Pro Thr Met Met Pro Gln Tyr Gln Gln Ala Phe
164                               530                               535                               540
165 Phe Gln Gln Gln Met Leu Ala Gln His Gln Pro Ser Gln Gln Gln Ala
166 545                               550                               555                               560
167 Ser Pro Glu Tyr Leu Thr Ser Pro Gln Glu Phe Ser Pro Ala Leu Val
168                               565                               570                               575
169 Ser Tyr Thr Ser Ser Leu Pro Ala Gln Val Gly Thr Ile Met Asp Ser
170                               580                               585                               590
171 Ser Tyr Ser Ala Asn Arg Gln Val Phe Phe Gln Ser Val Ala Asp Lys
172                               595                               600                               605
173 Glu Ala Ile Ala Asn Phe Thr Asn Gln Lys Asn Ile Ser Asn Pro Pro
174                               610                               615                               620
175 Asp Met Ser Gly Trp Asn Pro Phe Gly Glu Asp Asn Phe Ser Lys Leu
176 625                               630                               635                               640
177 Thr Glu Glu Glu Leu Asp Arg Glu Phe Asp Leu Leu Arg Ser Asn
178                               645                               650                               655
179 Arg Leu Glu Glu Arg Ala Ser Ser Asp Lys Asn Val Asp Ser Leu Ser
180                               660                               665                               670
181 Ala Pro His Asn His Pro Pro Glu Asp Pro Phe Gly Ser Val Pro Phe
182                               675                               680                               685
183 Ile Ser His Ser Gly Lys Gly Ser Pro Glu Lys Lys Ala Glu His Ser
184                               690                               695                               700
185 Ser Ile Asn Gln Glu Asn Gly Thr Ala Asn Pro Ile Lys Asn Gly Lys
186 705                               710                               715                               720
187 Thr Ser Pro Ala Ser Lys Asp Gln Arg Thr Gly Lys Lys Thr Ser Val
188                               725                               730                               735
189 Gln Gly Gln Val Gln Lys Gly Asn Asp Glu Ser Glu Ser Asp Phe Glu
190                               740                               745                               750
191 Ser Asp Pro Pro Ser Pro Lys Ser Ser Glu Glu Glu Glu Gln Asp Asp
192                               755                               760                               765
193 Glu Glu Val Leu Gln Gly Glu Gln Gly Asp Phe Asn Asp Asp Asp Thr
194                               770                               775                               780
195 Glu Pro Glu Asn Leu Gly His Arg Pro Leu Leu Met Asp Ser Glu Asp
196 785                               790                               795                               800
197 Glu Glu Glu Glu Glu Lys His Ser Ser Asp Ser Asp Tyr Glu Gln Ala
198                               805                               810                               815
199 Lys Ala Lys Tyr Ser Asp Met Ser Ser Val Tyr Arg Asp Arg Ser Gly
200                               820                               825                               830
201 Ser Gly Pro Thr Gln Asp Leu Asn Thr Ile Leu Leu Thr Ser Ala Gln
202                               835                               840                               845
203 Leu Ser Ser Asp Val Ala Val Glu Thr Pro Lys Gln Glu Phe Asp Val
204                               850                               855                               860

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205 Phe Gly Ala Val Pro Phe Phe Ala Val Arg Ala Gln Gln Pro Gln Gln
206 865 870 875 880
207 Glu Lys Asn Glu Lys Asn Leu Pro Gln His Arg Phe Pro Ala Ala Gly
208 885 890 895
209 Leu Glu Gln Glu Glu Phe Asp Val Phe Thr Lys Ala Pro Phe Ser Lys
210 900 905 910
211 Lys Val Asn Val Gln Glu Cys His Ala Val Gly Pro Glu Ala His Thr
212 915 920 925
213 Ile Pro Gly Tyr Pro Lys Ser Val Asp Val Phe Gly Ser Thr Pro Phe
214 930 935 940
215 Gln Pro Phe Leu Thr Ser Thr Ser Lys Ser Glu Ser Asn Glu Asp Leu
216 945 950 955 960
217 Phe Gly Leu Val Pro Phe Asp Glu Ile Thr Gly Ser Gln Gln Gln Lys
218 965 970 975
219 Val Lys Gln Arg Ser Leu Gln Lys Leu Ser Ser Arg Gln Arg Arg Thr
220 980 985 990
221 Lys Gln Asp Met Ser Lys Ser Asn Gly Lys Arg His His Gly Thr Pro
222 995 1000 1005
223 Thr Ser Thr Lys Lys Thr Leu Lys Pro Thr Tyr Arg Thr Pro Glu Arg
224 1010 1015 1020
225 Ala Arg Arg His Lys Lys Val Gly Arg Arg Asp Ser Gln Ser Ser Asn
226 1025 1030 1035 1040
227 Glu Phe Leu Thr Ile Ser Asp Ser Lys Glu Asn Ile Ser Val Ala Leu
228 1045 1050 1055
229 Thr Asp Gly Lys Asp Arg Gly Asn Val Leu Gln Pro Glu Glu Ser Leu
230 1060 1065 1070
231 Leu Asp Pro Phe Gly Ala Lys Pro Phe His Ser Pro Asp Leu Ser Trp
232 1075 1080 1085
233 His Pro Pro His Gln Gly Leu Ser Asp Ile Arg Ala Asp His Asn Thr
234 1090 1095 1100
235 Val Leu Pro Gly Arg Pro Arg Gln Asn Ser Leu His Gly Ser Phe His
236 1105 1110 1115 1120
237 Ser Ala Asp Val Leu Lys Met Asp Asp Phe Gly Ala Val Pro Phe Thr
238 1125 1130 1135
239 Glu Leu Val Val Gln Ser Ile Thr Pro His Gln Ser Gln Gln Ser Gln
240 1140 1145 1150
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242 1155 1160 1165
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246 <211> LENGTH: 3704
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248 <213> ORGANISM: Homo sapiens
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253 gcccaagtgc gagggcgga gcggcggcgc agcggcgggg ggcggggctg gcggggccgg 180
254 ggccggggcc ggctgcggct ccggcggcgc gtccgtgggg gtccgggtgt tcgcggtcgg 240
255 ccgccaccag gtcaccctgg aagatcgct ggccgaaggt ggattctcca cagttttcct 300
256 cgtgcgtact cacggtggaa tccgatgtgc attgaagcga atgtatgtca ataacatgcc 360

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/509,422

DATE: 10/06/2004

TIME: 16:26:12

Input Set : A:\pto.amc.TXT

Output Set: N:\CRF4\10062004\J509422.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date